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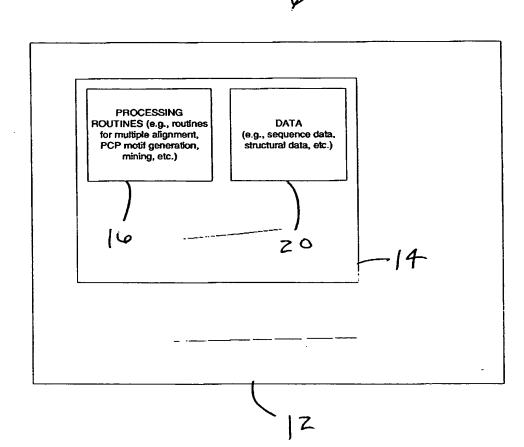
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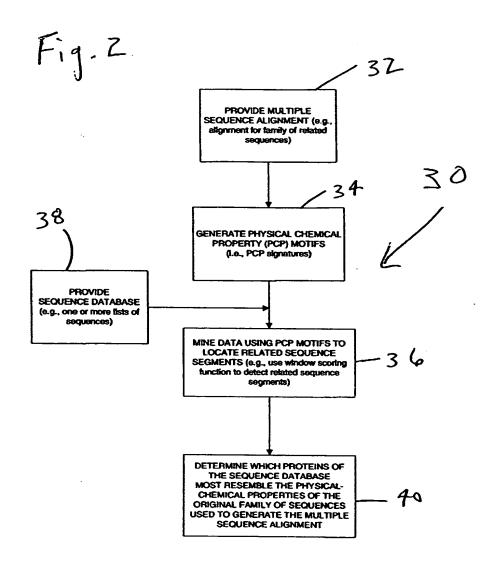
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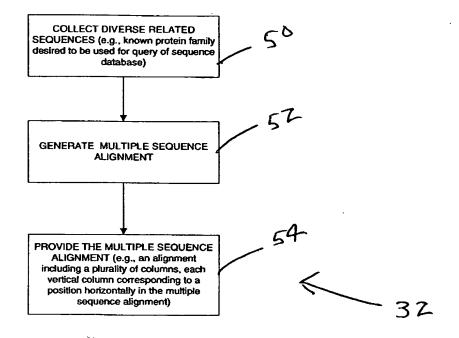


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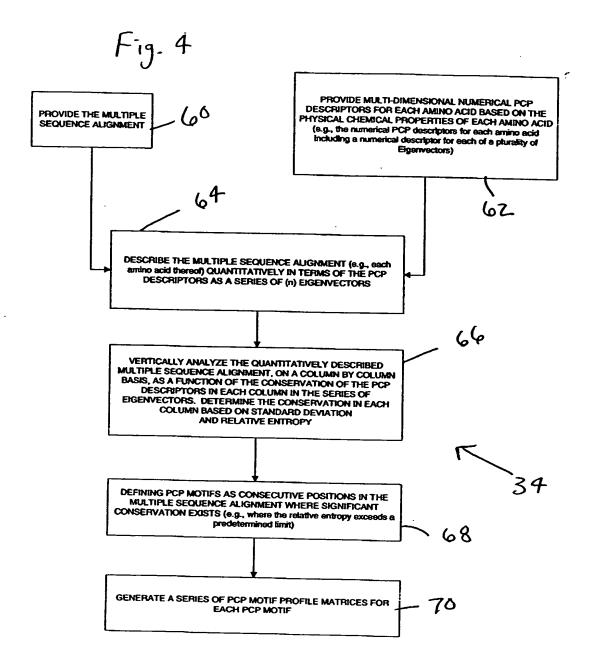


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Fig. 5 62 PROVIDE MULTI-DIMENSIONAL NUMERICAL PCP DESCRIPTORS FOR EACH AMINO ACID BASED ON THE PHYSICAL CHEMICAL PROPERTIES OF EACH AMINO ACID PROVIDE THE MULTIPLE SEQUENCE ALIGNMENT (e.g., the numerical PCP descriptors for each armino acid including a numerical descriptor for each of a plurality of Eigenvectors) DESCRIBE THE MULTIPLE SEQUENCE ALIGNMENT QUANTITATIVELY IN TERMS OF THE PCP DESCRIPTORS RESULTING IN (N) DISTINCT PCP DESCRIBED AUGMENTS CORRESPONDING TO THE N EIGENVECTORS, EACH DISTINCT ALIGNMENT INCLUDING COLUMNS CORRESPONDING TO THE COLUMNS (i.e., positions) OF THE MULTIPLE SEQUENCE ALIGNMENT, WHEREIN EACH COLUMN INCLUDES NUMERICAL 94 PCP DESCRIPTORS (i.e., corresponding to the eigenvector being defined) FOR EACH AMINO ACID (i.e., residue) IN THE COLUMN १५ ANALYZE EACH OF THE N PCP DESCRIBED ALIGNMENTS, COLUMN BY COLUMN, TO GENERATE CONSERVATION PROPERTY DATA FOR EACH COLUMN THEREOF (e.g., the conservation property data including the average value of each column and the related standard deviation for the column, and a relative entropy for the column) 34 88 SCANNING (e.g., horizontally across sequential columns that were analyzed) THE CONSERVATION PROPERTY DATA (e.g., the relative entropy values generated for each column of the PCP described 92 alignment being analyzed) TO DETECT CONSECUTIVE POSITIONS (e.g., corresponding to consecutively analyzed columns) WHERE THE RELATIVE ENTROPY EXCEEDS A PREDETERMINED LIMIT USER SPECIFIED GAP AND MINIMUM LENGTH LIMITS BASED ON THE DETECTED CONSECUTIVE POSITIONS AND USER SPECIFIED GAP AND MINIMUM LENGTH LIMITS, DETERMINING WHERE THE PCP MOTIFS ARE LOCATED IN THE MULTIPLE SEQUENCE ALIGNMENT 90

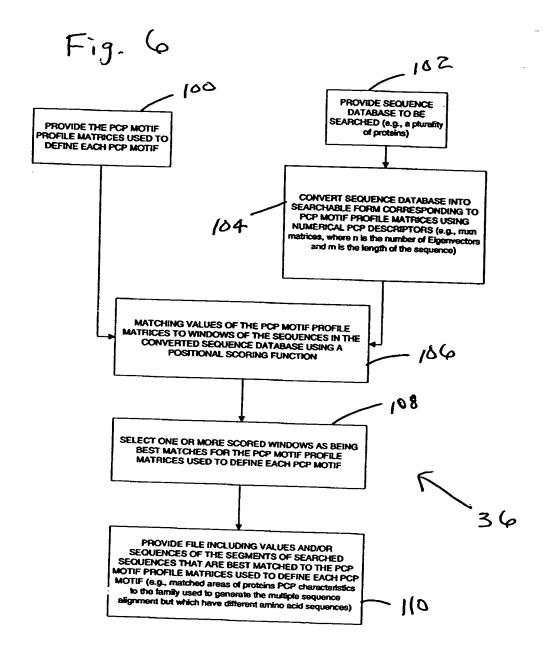
GENERATE A SERIES OF PCP MOTIF PROFILE MATRICES OR A MULTI-DIMENSIONAL MATRIX FOR EACH MOTIF (e.g., each motif defined by a plurality of matrices, with each matrix thereof corresponding to one of n eigenvectors, and further wherein each matrix includes a first level that includes average values for each

position in the PCP motif for the corresponding eigenvector and related standard deviation, and a second level that gives the relative entropy of each position of the PCP motif for the corresponding eigenvector)

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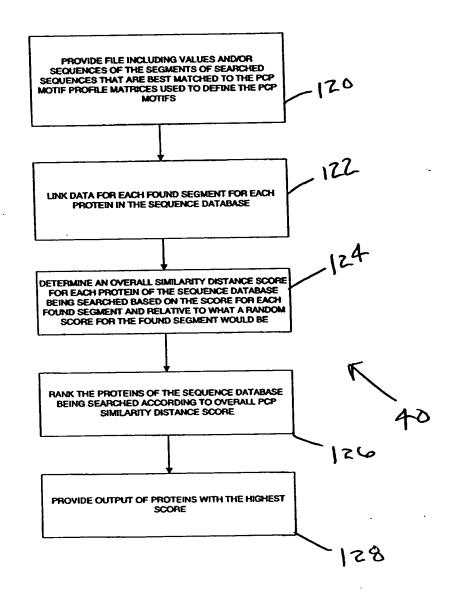
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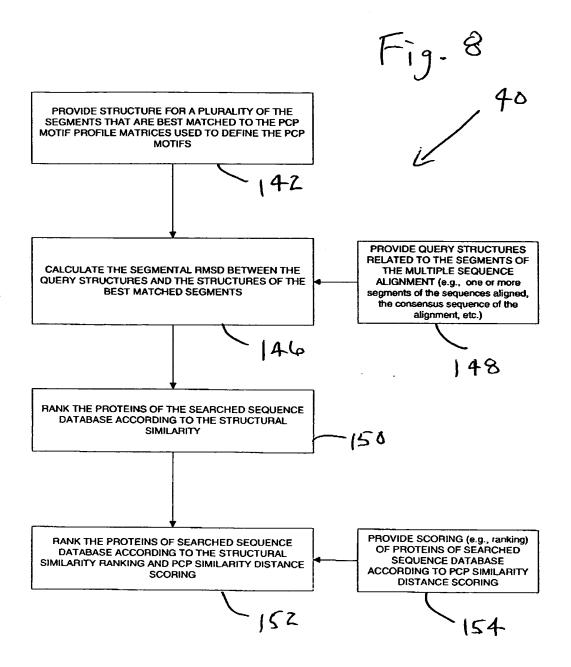


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Noti	· · ·	(S1)	(S2)	(S3)	(S4)	(S4) 42 APE score	ASTRAL40
	(Duman APE)					ave. ± std. dev	ave. ± std. dev
•	02 LNICS WN YDGLKA 74	0.91*	0.90*	0.63*	0.73*	0.87 ± 0.05	0.56 ± 0.05
2	89 PDILCLQETK 98	0.96*	0.93*	0.84*	0.70*	0.92 ± 0.04	0.61 + 0.07
ω	125 KEGYSGVGLLSRQCP 139	0.91*	0.86*	0.60	ر ا ا	0.85 + 0.06	0.64 + 0.05
^	יייייייייייייייייייייייייייייייייייייי				6	0.00 ± 0.00	0.03 ± 0.03
	143 GIGUEERDQEGRVIVAEFDSFVL 169 0.94*	0.94#	0.77*	0.71	0.81	0.84 ± 0.09	0.67 ± 0.07
S	171 YVPNA 175	0.96*	0.96*	0.68	0.86	0.94 ± 0.06	0 68 + 0 13
0	181 RLEYRQRW 188	0.80*	0.70*	0.78	0.77	074+006	0.67 ± 0.06
7	204 PLVI CGDI NVAH 214		•				0.00 H 0.00
•		0.90	0.88	0.82	0.78*	0.90 ± 0.04	0.55 ± 0.08
•	231 GF 1PQERQGFGEL 243	0.96*	0.91*	0.78	0.73	0.87 ± 0.09	0.70 ± 0.07
9	247 VPLADSFR 254	0.96*	0.93#	0.70	0.83	0.91 ± 0.08	0.74 ± 0.11
10	264 YTFWTYM 270	0.86*	0.77*	0.61	0.70	0.84 ± 0.08	0.61 ± 0.06
Ξ	274 RSKNVGWRLDYFLLSHSL 291	0.92*	0.89*	0.56	o 2	0.90 ± 0.04	0 54 + 0 07
12	306 GSDHCPI 312	0.93*	0.94*	0.88*	0.83*	0.92 ± 0.03	0.52 ± 0.09

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PDB	Score in bits	Motifs found	SCOP,	EC	Description
	the highest				
IHD7	score) 1942 (1.00)	1.2.3.4.5.6.7.8.9.10.11.12	1 1 151 P	A > 00 10	ADD
IAKO	1861 (00)	1,2,3,4,3,6,7,8,9,10,11,12	d.151.1.1	4.2.99.18	APE
	1001 (0.96)	1,2,3,4,5,7,8,9,10,11,12	d.151.1.1	3.1.11.2	Exonuclease III
2DNJ	1094 (0.56)	2,6,7,12	d.151.1.1	0000	Describence in
119Y	1056 (0.54)	1.4.5.6.7.9.12	d 151 1 2	0000	Phone in the state of the state
1 B 3U	840 (0.43)	5.7.9.12	9 118 1 2		r nosphandy inositol phosphate Syn
IMDA	814 (0.42)	801113	1.70.1.6	0.0.0	regulatory domain of protein phos
Vav	707 (0.11)		0.07.2.1	1.4.99.3	 Methylamine dehydrogenase
I JIAI I	/9/ (0.41)	/,9,12	d.32,1.3	1.13.11.2	Catechol 2.3-dioxygenase
EKM	792 (0.41)	6,7,12	b.30.2.1	1.43.6	Conner amine ovidese
IYRG	737 (0.38)	2,9,12	c.10.1.2	0000	Chase DNA 1
1009	698 (0.36)	5,6,12	c.56.5.4	3 4 11 -	A minoposition
PDB cod	PDB code of the protein				, Hamopophoaso
3COP co	de and d.151.1 i	² SCOP code and d.151.1 is the DNasel superfamily code	de		
Enzyme o	commission clas	Enzyme commission classification number			

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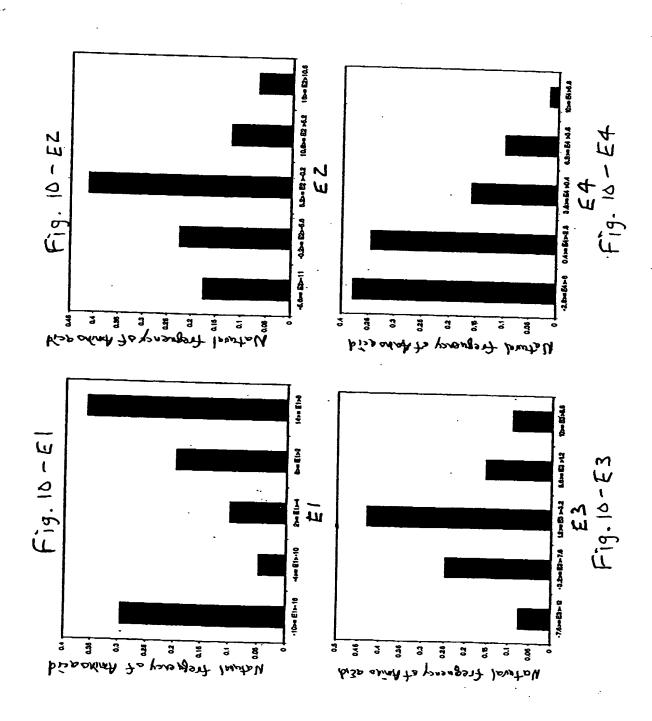
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PDB'	Score in bits (fraction to the highest	MOLEGOS found	SCOP ³	ВĊ	Description
1HD7	1942 (1,00)	1.2.3.4.5.6.7.8.9.10.11.12	J 151 1 1	3 20 10	
IAKO	1831 (0.94)	1,2,3,5,6,7,8,9,10,11,12	0.151.1.1	4.2.99.18	APE (Mn/Mg/Pb)
2DNJ	1072 (0.55)	1 3 5 5 7 0 10 10	1.1.1.1.1	3.1.11.2	Exonuclease III
1194	971 (0.50)	1 2 5 6 7 9 10 12	d.151.1.1	3.1.21.1	Deoxyribonuclease I
1009	698 (0.36)	5.6.9.10.12	0.101.1.2	3	Phosphatidylinositol phosphate Synaptojanin
IATL	633 (0.33)	5.6.9.10.12	400.0.4	3.4.1.1	Aminopepudase (Zn, Ca)
1D09	619 (0.32)	5.9.12	9 X8 2 1	0.1.61.16	Shake venom metalloprotease (Zn, Ca)
ID2N	613 (0.32)	5.6.8.9.12	C 37 1 13	1.1.0.1	Aspartate caroamoyitransferase (Zn)
IDOB	<i>579</i> (0.30)	2,5,9,12	c.10.2.1		Internalian I and it is in frequency in the internal in the internal in the internal
IEEM	571 (0.29)	5,6,8,12	a.45.1.1		Chitethione of the officers (Ca)
PDB ∞de	PDB code of the protein				Crammingto D-HattsTct 826
SCOP cod	le and d.151.1 is	SCOP code and d.151.1 is the DNasel superfamily code	de		
Enzyme o	ommission classi	Enzyme commission classification number			

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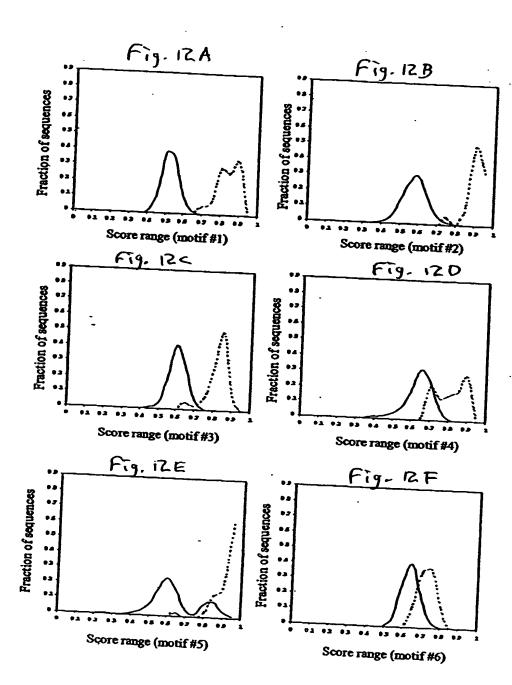
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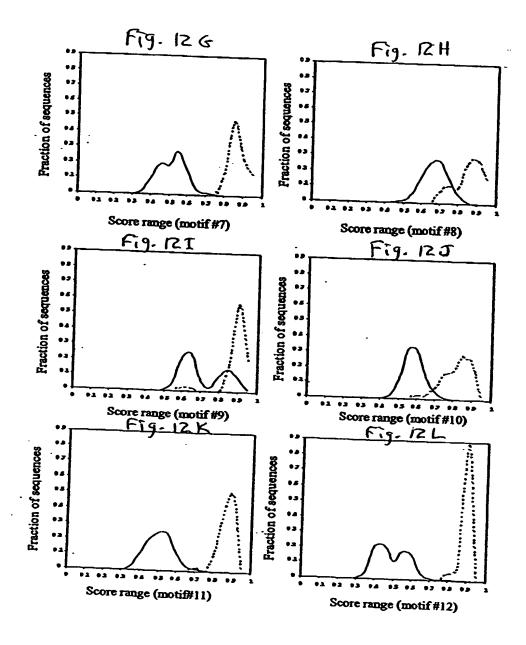


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